

# SEQUENCE LISTING

<110> Monia, Brett P.  
Gaarde, William A.  
Nero, Pamela S.

<120> Antisense Modulation of Focal Adhesion Kinase  
Expression

<130> ISPH-0533

<140>

<141>

<150> 09/377,310

<151> 1999-08-19

<150> PCT/US00/18999

<151> 2000-07-13

<160> 44

<170> PatentIn Ver. 2.0

<210> 1

<211> 3791

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (233)..(3391)

<300>

<303> DNA

<304> 12

<305> 9

<306> 823-830

<307> 1993-11

<308> L13616/Genbank

<309> 1995-01-02

<400> 1

cgaccactgt gagcccgagg cgtgaggcgt cgggaggaag cgcggctgct gtcgcccagc 60

gccgccccgt cgtcgtctgc cttegtttca cggcgccgag ccgcgggtccg agcagaactg 120

gggctccctt gcatctttca gttacaaatt cagtgccttc tgcagtttcc ccagagctcc 180

tcaagaataa cggaagggag aatatgacag atacctagca tctagcaaaa ta atg gca 238

Met Ala

1

gct gct tac ctt gac ccc aac ttg aat cac aca cca aat tcg agt act 286

Ala Ala Tyr Leu Asp Pro Asn Leu Asn His Thr Pro Asn Ser Ser Thr

5

10

15



aca ttt aga caa gcc aac ctt aat aga gaa gaa att ctg aaa 958  
 Thr Phe Arg Gln Phe Ala Asn Leu Asn Arg Glu Glu Ser Ile Leu Lys  
 230 235 240  
 ttc ttt gag atc ctg tct cca gtc tac aga ttt gat aag gaa tgc ttc 1006  
 Phe Phe Glu Ile Leu Ser Pro Val Tyr Arg Phe Asp Lys Glu Cys Phe  
 245 250 255  
 aag tgt gct ctt ggt tca agc tgg att att tca gtg gaa ctg gca atc 1054  
 Lys Cys Ala Leu Gly Ser Ser Trp Ile Ile Ser Val Glu Leu Ala Ile 18  
 260 265 270 36  
 ggc cca gaa gaa gga atc agt tac cta acg gac aag ggc tgc aat ccc 1102  
 Gly Pro Glu Glu Gly Ile Ser Tyr Leu Thr Asp Lys Gly Cys Asn Pro  
 275 280 285 290  
 aca cat ctt gct gac ttc act caa gtg caa acc att cag tat tca aac 1150  
 Thr His Leu Ala Asp Phe Thr Gln Val Gln Thr Ile Gln Tyr Ser Asn  
 295 300 305  
 agt gaa gac aag gac aga aaa gga atg cta caa cta aaa ata gca ggt 1198  
 Ser Glu Asp Lys Asp Arg Lys Gly Met Leu Gln Leu Lys Ile Ala Gly  
 310 315 320  
 gca ccc gag cct ctg aca gtg acg gca cca tcc cta acc att gcg gag 1246  
 Ala Pro Glu Pro Leu Thr Val Thr Ala Pro Ser Leu Thr Ile Ala Glu  
 325 330 335  
 aat atg gct gac cta ata gat ggg tac tgc cgg ctg gtg aat gga acc 1294  
 Asn Met Ala Asp Leu Ile Asp Gly Tyr Cys Arg Leu Val Asn Gly Thr  
 340 345 350  
 tcg cag tca ttt atc atc aga cct cag aaa gaa ggt gaa cgg gct ttg 1342  
 Ser Gln Ser Phe Ile Ile Arg Pro Gln Lys Glu Gly Glu Arg Ala Leu  
 355 360 365 370  
 cca tca ata cca aag ttg gcc aac agc gaa aag caa ggc atg cgg aca 1390  
 Pro Ser Ile Pro Lys Leu Ala Asn Ser Glu Lys Gln Gly Met Arg Thr  
 375 380 385  
 cac gcc gtc tct gtg tcagaa aca gat gat tat gct gag att ata gat 1438  
 His Ala Val Ser Val Ser Glu Thr Asp Asp Tyr Ala Glu Ile Ile Asp  
 390 395 400  
 gaa gaa gat act tac acc atg ccc tca acc agg gat tat gag att caa 1486  
 Glu Glu Asp Thr Tyr Thr Met Pro Ser Thr Arg Asp Tyr Glu Ile Gln  
 405 410 415  
 aga gaa aga ata gaa ctt gga cga tgt att gga gaa ggc caa ttt gga 1534  
 Arg Glu Arg Ile Glu Leu Gly Arg Cys Ile Gly Glu Gly Gln Phe Gly  
 420 425 430

gat gta cat caa att tat atg agt cca gag aat gct ttg gcg 1582  
Asp Val His Gln Gly Ile Tyr Met Ser Pro Glu Asn Pro Ala Leu Ala  
435 440 445 450  
gtt gca att aaa aca tgt aaa aac tgt act tcg gac agc gtg aga gag 1630  
Val Ala Ile Lys Thr Cys Lys Asn Cys Thr Ser Asp Ser Val Arg Glu  
455 460 465  
aaa ttt ctt caa gaa gcc tta aca atg cgt cag ttt gac cat cct cat 1678  
Lys Phe Leu Gln Glu Ala Leu Thr Met Arg Gln Phe Asp His Pro His  
470 475 480  
att gtg aag ctg att gga gtc atc aca gag aat cct gtc tgg ata atc 1726  
Ile Val Lys Leu Ile Gly Val Ile Thr Glu Asn Pro Val Trp Ile Ile  
485 490 495  
atg gag ctg tgc aca ctt gga gag ctg agg tca ttt ttg caa gta agg 1774  
Met Glu Leu Cys Thr Leu Gly Glu Leu Arg Ser Phe Leu Gln Val Arg  
500 505 510  
aaa tac agt ttg gat cta gca tct ttg atc ctg tat gcc tat cag ctt 1822  
Lys Tyr Ser Leu Asp Leu Ala Ser Leu Ile Leu Tyr Ala Tyr Gln Leu  
515 520 525 530  
agt aca gct ctt gca tat cta gag agc aaa aga ttt gta cac agg gac 1870  
Ser Thr Ala Leu Ala Tyr Leu Glu Ser Lys Arg Phe Val His Arg Asp  
535 540 545  
att gct gct cgg aat gtt ctg gtg tcc tca aat gat tgt gta aaa tta 1918  
Ile Ala Ala Arg Asn Val Leu Val Ser Ser Asn Asp Cys Val Lys Leu  
550 555 560  
gga gac ttt gga tta tcc cga tat atg gaa gat agt act tac tac aaa 1966  
Gly Asp Phe Gly Leu Ser Arg Tyr Met Glu Asp Ser Thr Tyr Tyr Lys  
565 570 575  
gct tcc aaa gga aaa ttg cct att aaa tgg atg gct cca gag tca atc 2014  
Ala Ser Lys Gly Lys Leu Pro Ile Lys Trp Met Ala Pro Glu Ser Ile  
580 585 590  
aat ttt cga cgt ttt acc tca gct agt gac gta tgg atg ttt ggt gtg 2062  
Asn Phe Arg Arg Phe Thr Ser Ala Ser Asp Val Trp Met Phe Gly Val  
595 600 605 610  
tgt atg tgg gag ata ctg atg cat ggt gtg aag cct ttt caa gga gtg 2110  
Cys Met Trp Glu Ile Leu Met His Gly Val Lys Pro Phe Gln Gly Val  
615 620 625  
aag aac aat gat gta atc ggt cga att gaa aat ggg gaa aga tta cca 2158  
Lys Asn Asn Asp Val Ile Gly Arg Ile Glu Asn Gly Glu Arg Leu Pro  
630 635 640

atg cct cca aat	cct cct acc ctc tac agc ctt	acg aaa tgc	2206
Met Pro Pro Asn Cys Pro Pro	Thr Leu Tyr Ser Leu Met Thr Lys Cys		
645	650	655	
tgg gcc tat gac ccc agc agg cgg ccc agg ttt act gaa ctt aaa gct			2254
Trp Ala Tyr Asp Pro Ser Arg Arg Pro Arg Phe Thr Glu Leu Lys Ala			
660	665	670	
cag ctc agc aca atc ctg gag gaa gag aag gct cag caa gaa gag cgc			2302
Gln Leu Ser Thr Ile Leu Glu Glu Glu Lys Ala Gln Gln Glu Glu Arg			
675	680	685	690
atg agg atg gag tcc aga aga cag gcc aca gtg tcc tgg gac tcc gga			2350
Met Arg Met Glu Ser Arg Arg Gln Ala Thr Val Ser Trp Asp Ser Gly			
695	700	705	
ggg tct gat gaa gca ccg ccc aag ccc agc aga ccg ggt tat ccc agt			2398
Gly Ser Asp Glu Ala Pro Pro Lys Pro Ser Arg Pro Gly Tyr Pro Ser			
710	715	720	
ccg agg tcc agc gaa gga ttt tat ccc agc cca cag cac atg gta caa			2446
Pro Arg Ser Ser Glu Gly Phe Tyr Pro Ser Pro Gln His Met Val Gln			
725	730	735	
acc aat cat tac cag gtt tct ggc tac cct ggt tca cat gga atc aca			2494
Thr Asn His Tyr Gln Val Ser Gly Tyr Pro Gly Ser His Gly Ile Thr			
740	745	750	
gcc atg gct ggc agc atc tat cca ggt cag gca tct ctt ttg gac caa			2542
Ala Met Ala Gly Ser Ile Tyr Pro Gly Gln Ala Ser Leu Leu Asp Gln			
755	760	765	770
aca gat tca tgg aat cat aga cct cag gag ata gca atg tgg cag ccc			2590
Thr Asp Ser Trp Asn His Arg Pro Gln Glu Ile Ala Met Trp Gln Pro			
775	780	785	
aat gtg gag gac tct aca gta ttg gac ctg cga ggg att ggg caa gtg			2638
Asn Val Glu Asp Ser Thr Val Leu Asp Leu Arg Gly Ile Gly Gln Val			
790	795	800	
ttg cca acc cat ctg atg gaa gag cgt cta atc cga cag caa cag gaa			2686
Leu Pro Thr His Leu Met Glu Glu Arg Leu Ile Arg Gln Gln Gln Glu			
805	810	815	
atg gaa gaa gat cag cgc tgg ctg gaa aaa gag gaa aga ttt ctg aaa			2734
Met Glu Glu Asp Gln Arg Trp Leu Glu Lys Glu Glu Arg Phe Leu Lys			
820	825	830	
cct gat gtg aga ctc tct cga ggc agt att gac agg gag gat gga agt			2782
Pro Asp Val Arg Leu Ser Arg Gly Ser Ile Asp Arg Glu Asp Gly Ser			
835	840	845	850

ctt cag ggt ccg gga aac caa cat ata tat cag gtg ggt aaa 2830  
 Leu Gln Gly Pro Ile Gly Asn Gln His Ile Tyr Gln Pro Val Gly Lys  
 855 860 865

cca gat cct gca gct cca cca aag aaa ccg cct cgc cct gga gct ccc 2878  
 Pro Asp Pro Ala Ala Pro Pro Lys Lys Pro Pro Arg Pro Gly Ala Pro  
 870 875 880

ggt cat ctg gga agc ctt gcc agc ctc agc agc cct gct gac agc tac 2926  
 Gly His Leu Gly Ser Leu Ala Ser Leu Ser Ser Pro Ala Asp Ser Tyr  
 885 890 895

aac gag ggt gtc aag ctt cag ccc cag gaa atc agc ccc cct cct act 2974  
 Asn Glu Gly Val Lys Leu Gln Pro Gln Glu Ile Ser Pro Pro Pro Thr  
 900 905 910

gcc aac ctg gac cgg tcg aat gat aag gtg tac gag aat gtg acg ggc 3022  
 Ala Asn Leu Asp Arg Ser Asn Asp Lys Val Tyr Glu Asn Val Thr Gly  
 915 920 925 930

ctg gtg aaa gct gtc atc gag atg tcc agt aaa atc cag cca gcc cca 3070  
 Leu Val Lys Ala Val Ile Glu Met Ser Ser Lys Ile Gln Pro Ala Pro  
 935 940 945

cca gag gag tat gtc cct atg gtg aag gaa gtc ggc ttg gcc ctg agg 3118  
 Pro Glu Glu Tyr Val Pro Met Val Lys Glu Val Gly Leu Ala Leu Arg  
 950 955 960

aca tta ttg gcc act gtg gat gag acc att ccc ctc cta cca gcc agc 3166  
 Thr Leu Leu Ala Thr Val Asp Glu Thr Ile Pro Leu Leu Pro Ala Ser  
 965 970 975

acc cac cga gag att gag atg gca cag aag cta ttg aac tct gac ctg 3214  
 Thr His Arg Glu Ile Glu Met Ala Gln Lys Leu Leu Asn Ser Asp Leu  
 980 985 990

ggt gag ctc atc aac aag atg aaa ctg gcc cag cag tat gtc atg acc 3262  
 Gly Glu Leu Ile Asn Lys Met Lys Leu Ala Gln Gln Tyr Val Met Thr  
 995 1000 1005 1010

agc ctc cag caa gag tac aaa aag caa atg ctg act gct gct cac gcc 3310  
 Ser Leu Gln Gln Glu Tyr Lys Lys Gln Met Leu Thr Ala Ala His Ala  
 1015 1020 1025

ctg gct gtg gat gcc aaa aac tta ctc gat gtc att gac caa gca aga 3358  
 Leu Ala Val Asp Ala Lys Asn Leu Leu Asp Val Ile Asp Gln Ala Arg  
 1030 1035 1040

ctg aaa atg ctt ggg cag acg aga cca cac tga gcctccccta ggagcacgtc 3411  
 Leu Lys Met Leu Gly Gln Thr Arg Pro His  
 1045 1050

ttgctaccct cttt ga tgttctctag ccttccacca gca gga attaaccctg 3471  
 tgtcctcagt cgccagcact tacagctcca acttttttga atgaccatct ggttgaaaaa 3531  
 tctttctcat ataagtttaa ccacactttg atttgggttc attttttgtt ttgttttttt 3591  
 caatcatgat attcagaaaa atccaggatc caaaatgtgg cgtttttcta agaataaaaa 3651  
 ttatatgtaa gcttttaagc atcatgaaga acaatttatg ttcacattaa gatacgttct 3711  
 aaagggggat ggccaagggg tgacatctta attcctaaac taccttagct gcatagtgga 3771  
 agaggagagc tagaagcaaa 3791

<210> 2  
 <211> 1052  
 <212> PRT  
 <213> Homo sapiens

<400> 2  
 Met Ala Ala Ala Tyr Leu Asp Pro Asn Leu Asn His Thr Pro Asn Ser  
 1 5 10 15  
 Ser Thr Lys Thr His Leu Gly Thr Gly Met Glu Arg Ser Pro Gly Ala  
 20 25 30  
 Met Glu Arg Val Leu Lys Val Phe His Tyr Phe Glu Ser Asn Ser Glu  
 35 40 45  
 Pro Thr Thr Trp Ala Ser Ile Ile Arg His Gly Asp Ala Thr Asp Val  
 50 55 60  
 Arg Gly Ile Ile Gln Lys Ile Val Asp Ser His Lys Val Lys His Val  
 65 70 75 80  
 Ala Cys Tyr Gly Phe Arg Leu Ser His Leu Arg Ser Glu Glu Val His  
 85 90 95  
 Trp Leu His Val Asp Met Gly Val Ser Ser Val Arg Glu Lys Tyr Glu  
 100 105 110  
 Leu Ala His Pro Pro Glu Glu Trp Lys Tyr Glu Leu Arg Ile Arg Tyr  
 115 120 125  
 Leu Pro Lys Gly Phe Leu Asn Gln Phe Thr Glu Asp Lys Pro Thr Leu  
 130 135 140  
 Asn Phe Phe Tyr Gln Gln Val Lys Ser Asp Tyr Met Leu Glu Ile Ala  
 145 150 155 160  
 Asp Gln Val Asp Gln Glu Ile Ala Leu Lys Leu Gly Cys Leu Glu Ile  
 165 170 175  
 Arg Arg Ser Tyr Trp Glu Met Arg Gly Asn Ala Leu Glu Lys Lys Ser  
 180 185 190  
 Asn Tyr Glu Val Leu Glu Lys Asp Val Gly Leu Lys Arg Phe Phe Pro

195							200								
Lys	Ser	Leu	Leu	Asp	Ser	Val	Lys	Ala	Lys	Thr	Leu	Arg	Lys	Leu	Ile
	210					215					220				
Gln	Gln	Thr	Phe	Arg	Gln	Phe	Ala	Asn	Leu	Asn	Arg	Glu	Glu	Ser	Ile
225					230					235					240
Leu	Lys	Phe	Phe	Glu	Ile	Leu	Ser	Pro	Val	Tyr	Arg	Phe	Asp	Lys	Glu
				245					250					255	
Cys	Phe	Lys	Cys	Ala	Leu	Gly	Ser	Ser	Trp	Ile	Ile	Ser	Val	Glu	Leu
			260					265					270		
Ala	Ile	Gly	Pro	Glu	Glu	Gly	Ile	Ser	Tyr	Leu	Thr	Asp	Lys	Gly	Cys
		275						280				285			
Asn	Pro	Thr	His	Leu	Ala	Asp	Phe	Thr	Gln	Val	Gln	Thr	Ile	Gln	Tyr
	290					295					300				
Ser	Asn	Ser	Glu	Asp	Lys	Asp	Arg	Lys	Gly	Met	Leu	Gln	Leu	Lys	Ile
305					310					315					320
Ala	Gly	Ala	Pro	Glu	Pro	Leu	Thr	Val	Thr	Ala	Pro	Ser	Leu	Thr	Ile
				325					330					335	
Ala	Glu	Asn	Met	Ala	Asp	Leu	Ile	Asp	Gly	Tyr	Cys	Arg	Leu	Val	Asn
			340					345					350		
Gly	Thr	Ser	Gln	Ser	Phe	Ile	Ile	Arg	Pro	Gln	Lys	Glu	Gly	Glu	Arg
		355						360				365			
Ala	Leu	Pro	Ser	Ile	Pro	Lys	Leu	Ala	Asn	Ser	Glu	Lys	Gln	Gly	Met
	370					375					380				
Arg	Thr	His	Ala	Val	Ser	Val	Ser	Glu	Thr	Asp	Asp	Tyr	Ala	Glu	Ile
385					390					395					400
Ile	Asp	Glu	Glu	Asp	Thr	Tyr	Thr	Met	Pro	Ser	Thr	Arg	Asp	Tyr	Glu
				405					410					415	
Ile	Gln	Arg	Glu	Arg	Ile	Glu	Leu	Gly	Arg	Cys	Ile	Gly	Glu	Gly	Gln
			420					425					430		
Phe	Gly	Asp	Val	His	Gln	Gly	Ile	Tyr	Met	Ser	Pro	Glu	Asn	Pro	Ala
		435						440				445			
Leu	Ala	Val	Ala	Ile	Lys	Thr	Cys	Lys	Asn	Cys	Thr	Ser	Asp	Ser	Val
	450					455					460				
Arg	Glu	Lys	Phe	Leu	Gln	Glu	Ala	Leu	Thr	Met	Arg	Gln	Phe	Asp	His
465					470					475					480
Pro	His	Ile	Val	Lys	Leu	Ile	Gly	Val	Ile	Thr	Glu	Asn	Pro	Val	Trp
				485					490					495	
Ile	Ile	Met	Glu	Leu	Cys	Thr	Leu	Gly	Glu	Leu	Arg	Ser	Phe	Leu	Gln
			500					505					510		
Val	Arg	Lys	Tyr	Ser	Leu	Asp	Leu	Ala	Ser	Leu	Ile	Leu	Tyr	Ala	Tyr
		515				520						525			
Gln	Leu	Ser	Thr	Ala	Leu	Ala	Tyr	Leu	Glu	Ser	Lys	Arg	Phe	Val	His
	530					535					540				

Arg	Asp	Ile	Ala		Arg	Asn	Val	Leu	Val	Ser	Ser		Asp	Cys	Val
545					550					555				560	
Lys	Leu	Gly	Asp	Phe	Gly	Leu	Ser	Arg	Tyr	Met	Glu	Asp	Ser	Thr	Tyr
				565					570					575	
Tyr	Lys	Ala	Ser	Lys	Gly	Lys	Leu	Pro	Ile	Lys	Trp	Met	Ala	Pro	Glu
			580					585					590		
Ser	Ile	Asn	Phe	Arg	Arg	Phe	Thr	Ser	Ala	Ser	Asp	Val	Trp	Met	Phe
		595					600					605			
Gly	Val	Cys	Met	Trp	Glu	Ile	Leu	Met	His	Gly	Val	Lys	Pro	Phe	Gln
	610					615					620				
Gly	Val	Lys	Asn	Asn	Asp	Val	Ile	Gly	Arg	Ile	Glu	Asn	Gly	Glu	Arg
625					630					635					640
Leu	Pro	Met	Pro	Pro	Asn	Cys	Pro	Pro	Thr	Leu	Tyr	Ser	Leu	Met	Thr
				645					650					655	
Lys	Cys	Trp	Ala	Tyr	Asp	Pro	Ser	Arg	Arg	Pro	Arg	Phe	Thr	Glu	Leu
			660					665					670		
Lys	Ala	Gln	Leu	Ser	Thr	Ile	Leu	Glu	Glu	Glu	Lys	Ala	Gln	Gln	Glu
		675					680					685			
Glu	Arg	Met	Arg	Met	Glu	Ser	Arg	Arg	Gln	Ala	Thr	Val	Ser	Trp	Asp
	690					695					700				
Ser	Gly	Gly	Ser	Asp	Glu	Ala	Pro	Pro	Lys	Pro	Ser	Arg	Pro	Gly	Tyr
705					710					715					720
Pro	Ser	Pro	Arg	Ser	Ser	Glu	Gly	Phe	Tyr	Pro	Ser	Pro	Gln	His	Met
				725					730					735	
Val	Gln	Thr	Asn	His	Tyr	Gln	Val	Ser	Gly	Tyr	Pro	Gly	Ser	His	Gly
			740					745					750		
Ile	Thr	Ala	Met	Ala	Gly	Ser	Ile	Tyr	Pro	Gly	Gln	Ala	Ser	Leu	Leu
		755					760					765			
Asp	Gln	Thr	Asp	Ser	Trp	Asn	His	Arg	Pro	Gln	Glu	Ile	Ala	Met	Trp
	770					775					780				
Gln	Pro	Asn	Val	Glu	Asp	Ser	Thr	Val	Leu	Asp	Leu	Arg	Gly	Ile	Gly
785				790						795					800
Gln	Val	Leu	Pro	Thr	His	Leu	Met	Glu	Glu	Arg	Leu	Ile	Arg	Gln	Gln
				805				810						815	
Gln	Glu	Met	Glu	Glu	Asp	Gln	Arg	Trp	Leu	Glu	Lys	Glu	Glu	Arg	Phe
			820					825					830		
Leu	Lys	Pro	Asp	Val	Arg	Leu	Ser	Arg	Gly	Ser	Ile	Asp	Arg	Glu	Asp
		835					840					845			
Gly	Ser	Leu	Gln	Gly	Pro	Ile	Gly	Asn	Gln	His	Ile	Tyr	Gln	Pro	Val
	850					855					860				
Gly	Lys	Pro	Asp	Pro	Ala	Ala	Pro	Pro	Lys	Lys	Pro	Pro	Arg	Pro	Gly
865					870					875					880
Ala	Pro	Gly	His	Leu	Gly	Ser	Leu	Ala	Ser	Leu	Ser	Ser	Pro	Ala	Asp
				885					890					895	

Ser Tyr Asn Glu Val Lys Leu Gln Pro Gln Glu Ser Pro Pro  
 900 905 910  
 Pro Thr Ala Asn Leu Asp Arg Ser Asn Asp Lys Val Tyr Glu Asn Val  
 915 920 925  
 Thr Gly Leu Val Lys Ala Val Ile Glu Met Ser Ser Lys Ile Gln Pro  
 930 935 940  
 Ala Pro Pro Glu Glu Tyr Val Pro Met Val Lys Glu Val Gly Leu Ala  
 945 950 955 960  
 Leu Arg Thr Leu Leu Ala Thr Val Asp Glu Thr Ile Pro Leu Leu Pro  
 965 970 975  
 Ala Ser Thr His Arg Glu Ile Glu Met Ala Gln Lys Leu Leu Asn Ser  
 980 985 990  
 Asp Leu Gly Glu Leu Ile Asn Lys Met Lys Leu Ala Gln Gln Tyr Val  
 995 1000 1005  
 Met Thr Ser Leu Gln Gln Glu Tyr Lys Lys Gln Met Leu Thr Ala Ala  
 1010 1015 1020  
 His Ala Leu Ala Val Asp Ala Lys Asn Leu Leu Asp Val Ile Asp Gln  
 025 1030 1035 1040  
 Ala Arg Leu Lys Met Leu Gly Gln Thr Arg Pro His  
 1045 1050

<210> 3  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> antisense sequence

<400> 3  
 ccgcgggctc acagtgggtcg

20

<210> 4  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> antisense sequence

<400> 4  
 ggcgccgtga agcgaaggca

20

<210> 5  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> antisense sequence

<400> 5

cagttctgct cggacggg

20

<210> 6  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 6  
gaaactgcag aaggcactga

20

<210> 7  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> antisense sequence

<400> 7  
ttctcccttc cggtattctt

20

<210> 8  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 8  
ctagatgcta ggtatctgtc

20

<210> 9  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 9  
ttttgctaga tgctaggtat

20

<210> 10  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 10

ggtaagcagc tgcc tt 20

<210> 11  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 11  
agtaccagg tgagtcttag 20

<210> 12  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 12  
cctgacatca gtagcatctc 20

<210> 13  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 13  
gttggcttat cttcagtaaa 20

<210> 14  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 14  
ggtagggat ggtgccgtca 20

<210> 15  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 15

tgttggtttc caat cc

20

<210> 16  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 16  
ctaggggagg ctcagtgtgg

20

<210> 17  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 17  
attcctcgct gctggtggaa

20

<210> 18  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> antisense sequence

<400> 18  
tttcaaccag atggtcattc

20

<210> 19  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 19  
ttctgaatat catgattgaa

20

<210> 20  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 20

catgatgctt aaaacac

20

<210> 21  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 21  
aatgtgaaca taaattgttc

20

<210> 22  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 22  
aaggtagttt aggaattaag

20

<210> 23  
<211> 15  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 23  
gcgggctcac agtgg

15

<210> 24  
<211> 15  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 24  
cgccgtgaag cgaag

15

<210> 25  
<211> 15  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 25

gttctgctcg gacc

15

<210> 26  
<211> 15  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 26  
aactgcagaa ggcac

15

<210> 27  
<211> 15  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 27  
ctcccttccg ttatt

15

<210> 28  
<211> 15  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 28  
agatgctagg tatct

15

<210> 29  
<211> 15  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 29  
ttgctagatg ctagg

15

<210> 30  
<211> 15  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 30

taagcagctg ccat

15

<210> 31  
<211> 15  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 31  
taccaggtg agtct

15

<210> 32  
<211> 15  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 32  
tgacatcagt agcat

15

<210> 33  
<211> 15  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 33  
tggcttatct tcagt

15

<210> 34  
<211> 15  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 34  
ttagggatgg tgccg

15

<210> 35  
<211> 15  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 35

ttggtttcca atcg

15

<210> 36  
<211> 15  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 36  
aggggaggct cagtg

15

<210> 37  
<211> 15  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 37  
tcctcgctgc tggtg

15

<210> 38  
<211> 15  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 38  
tcaaccagat ggtca

15

<210> 39  
<211> 15  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 39  
ctgaatatca tgatt

15

<210> 40  
<211> 15  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 40

tgatgcttaa aagct

15

<210> 41  
<211> 15  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 41  
tgtgaacata aattg

15

<210> 42  
<211> 15  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense sequence

<400> 42  
ggtagtttag gaatt

15

<210> 43  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> control sequence

<400> 43  
ttttaatcat attggtattc

20

<210> 44  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> control sequence

<220>  
<221> unsure  
<222> (1) .. (20)

<400> 44  
nnnnnnnnnn nnnnnnnnnn

20